

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- sub D17
- (i) APPLICANT: Zsebo, Krisztina M.  
Bosselman, Robert A.  
Suggs, Sidney V.  
Martin, Francis H.
  - (ii) TITLE OF INVENTION: Stem Cell Factor
  - (iii) NUMBER OF SEQUENCES: 104
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
    - (B) STREET: 5300 Sears Tower, 233 South Wacker Drive
    - (C) CITY: Chicago
    - (D) STATE: Illinois
    - (E) COUNTRY: United States of America
    - (F) ZIP: 60606-6402
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER:
    - (B) FILING DATE:
    - (C) CLASSIFICATION:
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 08/449,649
    - (B) FILING DATE: 24-MAY-1995
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 07/982,255
    - (B) FILING DATE: 25-NOV-1992
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 07/589,701
    - (B) FILING DATE: 01-OCT-1990
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 07/573,616
    - (B) FILING DATE: 24-AUG-1990
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 07/537,198
    - (B) FILING DATE: 11-JUN-1990
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 07/422,383
    - (B) FILING DATE: 16-OCT-1989
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Clough, David W.
    - (B) REGISTRATION NUMBER: 36,107
    - (C) REFERENCE/DOCKET NUMBER: 01017/32953A
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: 312/474-6300
    - (B) TELEFAX: 312/474-0448

(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 165 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu	Glu	Ile	Cys	Arg	Asn	Pro	Val	Thr	Asp	Asn	Val	Lys	Asp	Ile	Thr	
1				5					10					15		
Lys	Leu	Val	Ala	Asn	Leu	Pro	Asn	Asp	Tyr	Met	Ile	Thr	Leu	Asn	Tyr	
			20					25					30			
Val	Ala	Gly	Met	Asp	Val	Leu	Pro	Ser	His	Cys	Trp	Leu	Arg	Asp	Met	
		35					40					45				
Val	Thr	His	Leu	Ser	Val	Ser	Leu	Thr	Thr	Leu	Leu	Asp	Lys	Phe	Ser	
	50					55					60					
Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Gly	
65					70					75					80	
Lys	Ile	Val	Asp	Asp	Leu	Val	Ala	Cys	Met	Glu	Glu	Asn	Ala	Pro	Lys	
				85					90					95		
Asn	Val	Lys	Glu	Ser	Leu	Lys	Lys	Pro	Glu	Thr	Arg	Asn	Phe	Thr	Pro	
			100					105					110			
Glu	Glu	Phe	Phe	Ser	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	
		115					120					125				
Phe	Met	Val	Ala	Ser	Asp	Thr	Ser	Asp	Cys	Val	Leu	Ser	Ser	Thr	Leu	
	130					135					140					
Gly	Pro	Glu	Lys	Asp	Ser	Arg	Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	
145					150					155					160	
Pro	Pro	Val	Ala	Ala												
				165												

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 26 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:  
    (A) NAME/KEY: modified\_base  
    (B) LOCATION: 9  
    (D) OTHER INFORMATION: /mod\_base= Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACRTTYTTNG GNGCRTTYTC YTCCAT

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: modified\_base
  - (B) LOCATION: 11 & 14
  - (D) OTHER INFORMATION: /mod\_base= Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AARAAATCYT CNGGNGTRAA RTT

23

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTYYTCNGGYT TYTT

14

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGARGARA AYCCCCCAA RAYGT

26

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCNAAYGAYT AYATGWTMAC

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGNGGNARCA TRAANGGYTT

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACCAKAARAT CTTYAAANCG ATC

23

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTATTTTCAA TAGATCCATT GA

22

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAACTATGT CGCC

14

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTAGTCAAGC TGACTGATAA G

21

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAACCAACAA TGACTAGGCA A

21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTCCAGAGTC AGTGTC

16

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGAAGCTTG CCTTTCCTTA TGAAGAAGA

29

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGCCGCGGT TACGGTGGTA ACATGAAGGG CTTTGTGA

38

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
GATAAATGCA AGTGATAATC C 21

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
GCGGTCGACC CGCGGAAC TT TAAGTCCATG CAACAC 36

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:  
CACCCGCGGT TATGCAACAG GGGGTAACAT AAATGG 36

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:  
CACCCGCGGT TAGGCTGCAA CAGGGGGTAA CATAAA 36

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:  
CTTAATGTTG AAGAAACC 18

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GATGGTAGTA CAATTGTCAG AC

22

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTCTGACAAT TGTACTACCA TC

22

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAATTTAGTG ACGTCTTTTA CA

22

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTAGATGAGT TTTCTTTCAC GCAC

24

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAATCATTCA AGAGCCCAGA ACCC

24

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACATCCATC CCGGGGAC

18

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGGCAATAT TTTAAGTCTC AAGAAGACC

29

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCGCCGCGGC TCCTATAGGT GCTAATTGG

29

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTCACCCT GTTTGTGCTG GATCGCA

27

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:  
GGTGTCTAGA CTTGTGTCTT CTTCATAAGG A 31

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:  
CCCCCCCCHGG 10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:  
TTTTTTTTTTT TTTTTTTTGG 20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:  
TTTTTTTTTTT TTTTTTTTAG 20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:  
TTTTTTTTTTT TTTTTTTTCG 20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTCGGCCGAT CAGGCCCCC CCCC

24

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

30

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGCCGGATAG GCCTCACNNN NNNT

24

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGCCGGATAG GCCTCAC

17

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4673 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(660..773, 1184..1246, 2053..2223, 2837..2993, 3692..3774)

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: join(720..773, 1184..1246, 2053..2223, 2837..2993, 3692..3774)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AAAGTATCTT TCTATTGGCG AAGGACATGT TTTCCCATAA GTGGTAAACA AACTGTCTGC	60
ACATAATAAT TATCTTGCTG CCGTAAAGAT TAGGTTAAAT TCTGCCTTCG ATCTAAAAAC	120
ACACCCTTCT GTCAATCCGA GGAGCAGTGT GCTAGTCTAG AGGTCTAAAT GAAGGCTCCT	180
TTCACGGTTG TATTTCTGCT CCCCAAATTG TCCACATTTA AAAGGAGAGT GCTTCTTTTC	240
AGCCTTAGGC TCTGAATTTT ATGCATTCCT CCATTTTCCG AGGTCCCCCC CAAGTGATAA	300
TTCTGTTCACA CGTTGCTACA AGTTCATCCC TAATTGCCGT CAAGAACTG ACTGTAGAAG	360
GCTTACCACA GACGTTGTAA CCGACAGTAA AGCCATTGAA AGAGTAATTC AAACAGGATG	420
GAAGCCAGGA GTATTTTGTG GCTGTTGCTC TTTTCTTTT CAGTTTGGTG AGAGCAGCTT	480
GAATGCTTAA CATTAAAGCC ATCAGCTTAA AACAAAACAA AACAAAACAA AAAAAAACCC	540
CGCTCTGGCA TATTTGCACT TAACACATAC GGTATAAGGT GTTACTGGTT TGCATAGTTC	600
TGGATTTTTT TTTTTTAAAA ACTGATGGAC ACCAAGAAAT GTTCTGTTC TTTGTTTAG	659
ACT TGG ATT ATC ACT TGC ATT TAT CTT CAA CTG CTC CTA TTT AAT CCT	707
Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro	
-20 -15 -10 -5	
CTC GTC AAA ACT CAG GAG ATC TGC AGG AAT CCT GTG ACT GAT AAT GTA	755
Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val	
1 5 10	
AAA GAC ATT ACA AAA CTG GTAAGTAAAG AATGATTTTG GCATCTATAA	803
Lys Asp Ile Thr Lys Leu	
15	
GTCTTCCCTG TGCTTGCTGA CCACATAGGT TCAGGGCACT CCCGACAGGA GTTCCCAGCT	863
TTCTAAGATA AGGAATCACT GTACGAGTCT GAAGTGCTTC TTCTGGGCAA ATGGGAGATG	923
CTTAGGTCAT GGAGGGTTTA TCTGTATAAC TGGCCCTTTG CACACCAACA AAGTGA CTGA	983
CTGGCTTTTG CCTGTTACCT ACTGTCTCCA GTCCTGGGCA TGGTATATAC TTAGGCACCC	1043
AAGATTGGAT TTACAACTCA AGCATTATAT ATTGGACAAC ACGGGGTATG AGATATTAAT	1103
GATATGTCAG GTTGGATGGA TGAGTTTCT CAAGAAATTC TCTTGATTTT ACTCACGTTT	1163
TCATTTCTTG GTCTCTGTAG GTG GCG AAT CTT CCA AAT GAC TAT ATG ATA	1213
Val Ala Asn Leu Pro Asn Asp Tyr Met Ile	
20 25	
ACC CTC AAC TAT GTC GCC GGG ATG GAT GTT TTG GTATGTAGTC CACACACTTC	1266
Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu	
30 35	
TGAGTTGCCT TTTAGTAGCT AATGGGTGAC CTGTGCTTAT TCACATTGAA GACATTATTT	1326
GCTCTTTGTC GTTTTTAGAT GTTGACCTAT AATTTTCTCT TCAAGCTGCT GCTAAGATTA	1386
TCAGTGAGCA TTTCAGTATG TGTTTAAAGC CTA CTACTCATTA AAAGGAAATG GCTCATCTTA	1446

GACGTAGCAA CCGATGTTAA TTTTCCCCCA GGCATCTCTC AGAGGGACTT GAATGTTAAA	1506
ATCATGTTAA ATTTCCCTCCT TGGCTATGTT ATTTCTCATG GCTATGTTAT TCCTATTCGT	1566
ATTTTCATTTA AAGGGACGGA ATATTTATTG TATTTCTGAA CTTTTTCAGG CATGCATCCG	1626
GGTCTTTGAA TAAAACACTA AGACTCCCTC TAGTAATGTT TGTAATCCTG TCTGTATCGA	1686
ATGTCTTTGA AAACGCAGTG ACTAAGCCAT AAATAATCTT CCACAGAACG TCCAGTGGTT	1746
CATGAACTTT GTATGTGGGG GTGGGGCAAG AATTGTCTCA CTATTGGTCA AGGAAGAGAA	1806
GGTAAGGTAT GCAAGGGTGG TTTAATCTTC TTCCGTGGAA GGACAAAATC ATCTATCATT	1866
TCCTCTGATC TCTATGCATT TGTTTGTTTT GAACCTGAATC TGACTTGAGC AAGAGTTGGC	1926
GTCCTGTGTT CTGAGGAAAC TCTTTGTCCT GCAGTCAGTG ACTAAAAGTG CTGAGAGATC	1986
TGAAGAGCAC TCTGAATCTG CCATATTTTT AATAGATGCT TTGTCTTCTC TTTGAATTTT	2046
TTCCAG CCT AGT CAT TGT TGG TTA CGA GAT ATG GTA ACA CAC TTA TCA	2094
Pro Ser His Cys Trp Leu Arg Asp Met Val Thr His Leu Ser	
40 45 50	
GTC AGC TTG ACT ACT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC	2142
Val Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly	
55 60 65	
TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GGG AAA ATA GTG GAT GAC	2190
Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp	
70 75 80 85	
CTC GTG GCA TGT ATG GAA GAA AAT GCA CCT AAG GTAACCTGGT ATTCATCAGA	2243
Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys	
90 95	
ATTATTTTTT TTATACTGAG CTCATGATGA GCAATTCACA ACCACTTGTA ATTCCAGCTC	2303
CAGAGGACAT TATCCCCTCT TTGGATGCCA TAGGAATCTG CTCTCAAATA TGTAGATACC	2363
ACCTCTGCCA CCTCAGCACA TACATACACA TAATTAAAAA ATAGAAACAT TAAAGGAGTT	2423
CCAATCAATC CTTATTCTTT TCTGTATTCA GTATGCCCAG ATGTAAATTC TAGGAATATG	2483
TTTTAAAGGC TAATTCCTTAT TTTGTAATAA GCAGCTTTAA AATTCCTTAAT TGTTTTTTTCG	2543
GGTCACTTTA TTGTCCTATT GCCACGACAT TGTCTGTGCC CATTGTCTGT TATTCCTTCT	2603
GTTTTGTTTA TTGTTCCCTA GTTACTTTGA TCATGAGATT GACCTGTTAC CCGTTGTTAT	2663
TCTCTGTAGC CATTTTGAGT TGTGTCTATT AGAACAGCTG TTAAATTACT TGAATCATTG	2723
AGGACATAGT CAATAATCTA TTATGCTGAT CCAGTCAAGT CTATGAGTTA TTTGAAAAC	2783
AGAATCTTTG TTAATTATTT GTTTGCTTGT TTGTTTGTTT ATTATTTGTC TAG AAT	2839
Asn	
GTA AAA GAA TCA CTG AAG AAG CCA GAA ACT AGA AAC TTT ACT CCT GAA	2887
Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu	
100 105 110	
GAA TTC TTT AGT ATT TTC AAT AGA TCC ATT GAT GCC TTC AAG GAC TTC	2935
Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe	
115 120 125	

ATG GTG GCA TCT GAC ACT AGT GAT TGT GTG CTC TCT TCA ACA TTA GGT Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu Gly 130 135 140 145	2983
CCT GAG AAA G GTAAGGCTTT TAAGCATTTC TTGTTTAAAT GTACATAGAA Pro Glu Lys	3033
AGCCTGAACT TCTGTAAGCC TCTACTGCTG AATCAACTAA ATGTGTTGCT GTAGAAAGAA	3093
CGTGTGGGTT TTTCTGATAA AAACAAAAAG CAAATATCAA TGACTIONCAA TGATTATTAT	3153
CTAGCTTGAG AGATATGCCC TAAGACAGCG ATTCTCGATA TTTCTAAATT AAAGAATTGT	3213
GTGATGGTGG CTCACATATT TTCTAACTGT GATATTTGCC AGGAGAGTAG AATAATGTTA	3273
TTCTTCATCC CCAGAATTCC TAAGATTTC ACGTCTCATGT CTTTTCCATA AGGTTCAAAC	3333
TCTGAGACTT GAGTTCTGAG CCTCAGCAGG TCATTCTGAA TCCCCACTCT CCCCAGCTG	3393
GGTCCCTATG GGGGAACTAA CTTTCATTGCT TTCTTTTAAA ACATGACGAG TTACCAACAG	3453
CTCCTCGCTA TTATAACAT GTTCCTAAGC ATGTCTGTGC ATGCAATAAG CCTTCACTCT	3513
ACAAGACAGT TATGGTGTAT CGCTTGACAA AACTGAGCAG CCAAGCTGAG TATGAAATAA	3573
TAATCTAGAC TTGGGAGGCA GACCCAGCAC CTACTGTGAT ATTGCACTTC GCCTTTGGGG	3633
GACTCTATGA TTCAAAGTT CACCATGTAA CACTGACACA TTATTGCTTT CTATTTAG AT Asp	3693
TCC AGA GTC AGT GTC AGA AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC Ser Arg Val Ser Val Arg Lys Pro Phe Met Leu Pro Pro Val Ala Ala 150 155 160 165	3741
AGT TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGTAAGTACA CATATCTGAT Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn 170 175	3794
TTACTGCATG CATGGCTCCA AGTATCCTCT ATAGGAGTGT TGCATGGACT TAAAGTTTAT	3854
AAATCACTAC TAATAATGCT GTTCTGTCAC TGTTATTCCCT TGTATGGGCT TCCTGACAAT	3914
TAAATATCTG GTTTGTAGAA TCGGATCTCC TTAGAGGTTA AGATGACCAT GACAAAATTA	3974
GGCCAATCAA CTTTCTGCGA AGGTTATTTT AAATAAGGCA CGAAATTAAT TGAAGGAAAA	4034
AAAAATACAA GCAAGGCCTT ATTTTGAATC ATGGTAGGCT TAAAATAGAC TTTGTGGAGA	4094
ATGTCCCTGA TCAAAGTGGA GTTTTCAGAT TTCAAGTGCA TGTGCTAACT CTCCACAATG	4154
TCAAGGCTAT TTTCAGTTTT GTGTCTCCAT ATTTACTACT GCATGTTTGG AAATTTGCTG	4214
ATGCTGTTAG ATTACCTAAG AATGTATGTT GAAGAAGAAT GGACTIONCTTT CCCTAAAATT	4274
TCTGTCTCTT TTGCCCCAGA ACCCACGTTT CTGGAAGACT ATCTTATTTT CATGTCTGTG	4334
CAATGATCAT TATAAGATT ATTGAATATA CTGGGAATAC TCTGGTTTCT GTTTTTACAG	4394
ATTCATAATA GCTTATTCAG TCTTTAAAGA AAGTTCTCTG AAGTCCATGC TTTAGAATGT	4454
TTCTCTATCA AAACCTTGACC TGGACCTTAA ATAAAGCTAT ATTTAGTCTT TTTATCCCTG	4514
AAAAATATAT TTCACAGTGT AGACATTTGA TATACATCTA AGGGAAGGAT GCTGCCAGAA	4574

TGCTCGGGCT GGCAGTCTAC AAAGTCCACT GCTCTCAGGA TGGACTTCTG AAAGCGGAAA 4634  
TTGTGAACTG CATGCATATA ACATATCAGA TCCTCGAGC 4673

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 196 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Thr	Trp	Ile	Ile	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	Leu	Leu	Phe	Asn	Pro			
-20					-15				-10						-5			
Leu	Val	Lys	Thr	Gln	Glu	Ile	Cys	Arg	Asn	Pro	Val	Thr	Asp	Asn	Val			
			1					5					10					
Lys	Asp	Ile	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	Asn	Asp	Tyr	Met	Ile			
	15						20					25						
Thr	Leu	Asn	Tyr	Val	Ala	Gly	Met	Asp	Val	Leu	Pro	Ser	His	Cys	Trp			
	30					35					40							
Leu	Arg	Asp	Met	Val	Thr	His	Leu	Ser	Val	Ser	Leu	Thr	Thr	Leu	Leu			
	45					50				55					60			
Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile			
				65					70					75				
Asp	Lys	Leu	Gly	Lys	Ile	Val	Asp	Asp	Leu	Val	Ala	Cys	Met	Glu	Glu			
			80					85					90					
Asn	Ala	Pro	Lys	Asn	Val	Lys	Glu	Ser	Leu	Lys	Lys	Pro	Glu	Thr	Arg			
		95					100					105						
Asn	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Ser	Ile	Phe	Asn	Arg	Ser	Ile	Asp			
	110					115					120							
Ala	Phe	Lys	Asp	Phe	Met	Val	Ala	Ser	Asp	Thr	Ser	Asp	Cys	Val	Leu			
	125					130				135					140			
Ser	Ser	Thr	Leu	Gly	Pro	Glu	Lys	Asp	Ser	Arg	Val	Ser	Val	Arg	Lys			
			145						150					155				
Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	Leu	Arg	Asn	Asp	Ser			
			160					165						170				
Ser	Ser	Ser	Asn															
			175															

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 849 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 26..844

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 101..844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTGGATCGCA GCGCTGCCTT TCCTT	ATG AAG AAG ACA CAA ACT TGG ATT ATC	52
	Met Lys Lys Thr Gln Thr Trp Ile Ile	
	-25 -20	
ACT TGC ATT TAT CTT CAA CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT		100
Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro Leu Val Lys Thr		
-15 -10 -5		
CAG GAG ATC TGC AGG AAT CCT GTG ACT GAT AAT GTA AAA GAC ATT ACA		148
Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val Lys Asp Ile Thr		
1 5 10 15		
AAA CTG GTG GCG AAT CTT CCA AAT GAC TAT ATG ATA ACC CTC AAC TAT		196
Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr		
20 25 30		
GTC GCC GGG ATG GAT GTT TTG CCT AGT CAT TGT TGG TTA CGA GAT ATG		244
Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met		
35 40 45		
GTA ACA CAC TTA TCA GTC AGC TTG ACT ACT CTT CTG GAC AAG TTT TCA		292
Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Asp Lys Phe Ser		
50 55 60		
AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GGG		340
Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly		
65 70 75 80		
AAA ATA GTG GAT GAC CTC GTG GCA TGT ATG GAA GAA AAT GCA CCT AAG		388
Lys Ile Val Asp Asp Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys		
85 90 95		
AAT GTA AAA GAA TCA CTG AAG AAG CCA GAA ACT AGA AAC TTT ACT CCT		436
Asn Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro		
100 105 110		
GAA GAA TTC TTT AGT ATT TTC AAT AGA TCC ATT GAT GCC TTC AAG GAC		484
Glu Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp		
115 120 125		
TTC ATG GTG GCA TCT GAC ACT AGT GAT TGT GTG CTC TCT TCA ACA TTA		532
Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu		
130 135 140		
GGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA		580
Gly Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu		
145 150 155 160		
CCC CCT GTT GCA GCC AGT TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT		628
Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn		
165 170 175		
AGG AAA GCC GCA AAG TCC CCT GAA GAC CCA GGC CTA CAA TGG ACA GCA		676
Arg Lys Ala Ala Lys Ser Pro Glu Asp Pro Gly Leu Gln Trp Thr Ala		
180 185 190		

ATG GCA CTG CCG GCT CTC ATT TCG CTT GTA ATT GGC TTT GCT TTT GGA	724
Met Ala Leu Pro Ala Leu Ile Ser Leu Val Ile Gly Phe Ala Phe Gly	
195 200 205	
GCC TTA TAC TGG AAG AAG AAA CAG TCA AGT CTT ACA AGG GCA GTT GAA	772
Ala Leu Tyr Trp Lys Lys Lys Gln Ser Ser Leu Thr Arg Ala Val Glu	
210 215 220	
AAT ATA CAG ATT AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA CAG	820
Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Gln	
225 230 235 240	
AAA GAG AGA GAG TTT CAA GAG GTG TAATT	849
Lys Glu Arg Glu Phe Gln Glu Val	
245	

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu	
-25 -20 -15 -10	
Leu Leu Phe Asn Pro Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro	
-5 1 5	
Val Thr Asp Asn Val Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro	
10 15 20	
Asn Asp Tyr Met Ile Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu	
25 30 35	
Pro Ser His Cys Trp Leu Arg Asp Met Val Thr His Leu Ser Val Ser	
40 45 50 55	
Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser	
60 65 70	
Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val	
75 80 85	
Ala Cys Met Glu Glu Asn Ala Pro Lys Asn Val Lys Glu Ser Leu Lys	
90 95 100	
Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe	
105 110 115	
Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr	
120 125 130 135	
Ser Asp Cys Val Leu Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg	
140 145 150	
Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser	
155 160 165	
Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ala Lys Ser Pro	
170 175 180	



Glu Asp Pro Gly Leu Gln Trp Thr Ala Met Ala Leu Pro Ala Leu Ile  
 185 190 195  
 Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Lys  
 200 205 210 215  
 Gln Ser Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
 220 225 230  
 Asp Asn Glu Ile Ser Met Leu Gln Gln Lys Glu Arg Glu Phe Gln Glu  
 235 240 245  
 Val

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152  
 ..3307, 3513..3595)

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152  
 ..3307, 3513..3595)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CACAAGTGAG TAGGGCGCGC CCGGGAGCTC CCAGGCTCTC CAGGAAAAAT CGCGCCCCGGT	60
GCCCCGGGGA AGCCGGCGCT CCCTGGGACT TGCAGCTGGG GCGTGCAGGG CTGTGCCTGC	120
CGGGTGAGAT ACTACAAAGA TAAATCAGTT GCACAAGTTC TTGAAACTCT ACAGTGTAAT	180
AAGGAAAAAT AAGTCATGCA TAAAAGCAAC TATAATACAT AATAGAAAAT GTTATTTTCA	240
AGCCGATGTG TAGGTTATGT GTGTTTCGAGA GAGAGAGAGA GAAGACAGAT TACTTTCTGC	300
TAGGGTTCAA GAATGCCTTC CTGTTGGCTA AGGAAATATT TTCCTTAAGT GGCTAAAAAG	360
CTGTGTTTCA AAATATTCTT TTGATGTCTC ACAAATTCAG TGGAATTCTC TTAGGTCTAA	420
AAATATACAT CTCTCTCACT TTAACCTGGT GTGCTATTGT AGATTATTGG ATTAAAGCAC	480
TGCTCAGGGA TTATGCTGCT TCTTGCCAAG CAGTCTACAT TTAAAGTAGA AATAAGATGT	540
TTCTTTTGGT GCCATAAGGT ATACATTTTA TGCATTCTCT AGTTTTTAGA AGATACCCTA	600
AGGGCTAAGT CTTTAACATG CTGCTACAAG TTTATTCCTA ATTGCCATTG GGAAATTGGC	660
TGAAGAAAGT TTTTAACAAA AGTTAACAAAT ATTGTCATTG AGAGAATAAT TCAAAATGGA	720
TTTAACTAA AAGCTTTTAA AAACCTTGGT GAGCATAGCT TGAATGCGTA ATATTTAATT	780
GCATTTAAGC CAATAACATA TATTAGACTG GTCTTTTGT GCATCAAGGC ATTAGATGTT	840
AAAAGTTTGA ATGATTACAG ATCTTAACTG ATGATCACCA AGCAATTTT CTGTTTTTCAT	900

TTAG ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG CTG CTC CTA TTT AAT Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn -20 -15 -10	949
CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT CGT GTG ACT AAT AAT Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn -5 1 5 10	997
GTA AAA GAC GTC ACT AAA TTG GTAAGTAAGG AATGCTTTAC CGTGCTGTGT Val Lys Asp Val Thr Lys Leu 15	1048
AAAAAAGAGC TGTGGCTCTT TTTCCTGTGC TTGTTGATAA AAGATTTAGA TTTTCTTGC	1108
CCCAAAGTAA TGTTTTCCCTA AAGTGGGGAA AGTAATCACT GGGTTACAAT AAAGGGTTTA	1168
TAGAAAAGCAG GTAGTGAGAT ATTTAGGGTC ATGGATAATT TGTTGGTAAA ACTGGCTAGT	1228
TGCACACCAC TGCTGTGACT GCTTCTTTGC TGGTCTTCTC CCCATCCTTC ATAGGCAGTG	1288
AAGGACCTTG GAGAGTTCGC TGTGTGCTGA TGGGCTTGCC CCAGCTTGTT CCCATAATC	1348
TCTCCAGTGG GTTCCCAGC ATGTTCTATT CCCCTTCACA TGTCTTCCTA CTCTTCTTTA	1408
AAAAGCCTAA CGAAAGGAAA TCTGAAATGG CTATTCTCCC AATTCAATCA GCAGGAAGAC	1468
CCTGTACAT GTCAGTGGGT GTTTGCTCCT TCAGGGAACA TAGAGAGGTG ATTCATTGCC	1528
CACATGTTGA AGGGACTCAT CTCCCTGGTT TGTCACATTG AACTCTTCCC TCAGCGAAAG	1588
CATTTGCATT GCTTCCCGAA TTCCAAGATC ACAGGTGGAA GCTGAAATTC AGATCATGTT	1648
TCCAAAACCTC AGTAGGTTAT ACCTAGCCAG GCATAACTGA ATTTGGAGTC TAAAAGATCT	1708
GTATTATCAC TTTTTTATTT TGAAGGATGC CTTTGTGATTA CAGAGGAAA TCAAGGATTA	1768
AAAATCAATA TACATGTAAA TATTGAAATT CATTGGTAAC TTAAAAAGC ACAACAGTTT	1828
TGTGTGCTTT TCTCCAAAGC ACTACAAATA TGATTAATTG ATGTATAAGA ATTTTCTTAT	1888
GGAATTTTTT TTTTGTCTC TGTAG GTG GCA AAT CTT CCA AAA GAC TAC ATG Val Ala Asn Leu Pro Lys Asp Tyr Met 20 25	1940
ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT TTG GATGTAAAC Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu 30 35	1986
TACATTTCTG AGTTTCATTT TAGTAGCTCA TAGAAGAAAT GGGATCATTC ATATTGAGAT	2046
AGTACACTAG CTGCTATTTA GGAGCTTGCT TATTGTCAGG ATTTGAAGAA TTTATCTTTG	2106
GAATTTGACT TGCAGGCTTT TTTTCCCCC TCTTCTGTT ACAAGAGTCC CTCCTCCTAT	2166
TACAATAGTC CCTCCTCCTC CTGTCACACT AGTCCCTTCT CTTCTGTGTA CAATAACCCC	2226
TGTCCTCCTA TTACAACATT TTAAGTAATG TAATATTAAT TTAAAAATC TGGCCAGGCA	2286
CGGTGGTTCA TGCTTGTAAT CCCAGCACAT TGGGAAGCTG AGACGGGTGG ATCATTGAG	2346
GTCAGGAAGT TTGAGACAGC CTGGCCAACA TGGTGAACT TCCTCTCTAC TAAAAATAAA	2406
AAAGTAGCCA GGCATGGTGG CAGGCACTTG TAATCTGAGC TACTCGAGAG GCTGAGGCAG	2466
GAGAATCACT TGAGTAACTA AAACGATAGC TTTGAAGAGT ACTCCGAGTT TTATGGCACT	2526

TACTTATTAA AATAGCTGTT TTGTCTCTTT TTTCATATCT TGCAG CCA AGT CAT	2580
Pro Ser His	
40	
TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC AGC TTG ACT GAT	2628
Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser Leu Thr Asp	
45 50 55	
CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC	2676
Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser	
60 65 70	
ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG	2724
Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val Glu Cys Val	
75 80 85 90	
AAA GAA AAC TCA TCT AAG GTAACCTTGT GTTCATTGGG ATTATTTTTC	2772
Lys Glu Asn Ser Ser Lys	
95	
ATTACGCTTC TCTAAAAACC CATGCTTCTT GGTGCTGTTG GGGAAAATGA GGCACCTTTA	2832
TTTATGATAT TTGATTGTA TAAACTTCAA ATTTAAAAAT CTTGTTTCTGAG TGAGCAAAGA	2892
AAACAAGTAT TTGCAGTTAT ACTGCAATAC TGAAGTGCAC ATTCTTGTGT TCACTGCCCC	2952
AGATTCAACT TGTGATCCCA CTGGGATCAC TACCCTGCAT TACCAATCTG AATTACATAC	3012
GTAAAAACAG CCATCTAAAA GTGCTAGTTG TAAGAGTCTA AATACTTGAA TCTTTGAGAG	3072
ACATATTTTAT AGTCCATTAT CTTACCTCA GTTAAGTCTG AAGACTATTT GAAAAATGTA	3132
ATCCTATTTT TTCTTCTAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC	3184
Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro	
100 105	
AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT	3232
Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile	
110 115 120	
GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG	3280
Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val	
125 130 135	
GTT TCT TCA ACA TTA AGT CCT GAG AAA GGTAAGACAT GTAAGCATTT	3327
Val Ser Ser Thr Leu Ser Pro Glu Lys	
140 145	
CCAGTTCAAA TGTAACAAC AAACCTTAAAT CTTCCCTATG TAGTAAGAAT CTACCTCTGT	3387
GTAAAGCTGT AGCAAGATAC ATGCATGTAC GTCTAATAAA AAAGCAGATA TCAATAGCAC	3447
AGAAGAACT CTATAACTCA TACAAATCAC CATATAACAC TGACACATTA TTGCTTTCTA	3507
TTTAG ATT CCA GAG TCA GTG TCA CAA AAC CAT TTA TGT TAC CCC CTG	3554
Ile Pro Glu Ser Val Ser Gln Asn His Leu Cys Tyr Pro Leu	
150 155 160	
TTG CAG CCA GCT CCC TTA GGA ATG ACA GCA GTA GCA GTA ATAGTAAGTA	3603
Leu Gln Pro Ala Pro Leu Gly Met Thr Ala Val Ala Val	
165 170 175	
CATATATCTG ATTTAATGCA TGCATGGCTC CAATTAGCAC CTATAGGAGT ATTGCATGGG	3663
CTTTCAAGGA AACTTCTACA TTTATTATTA TTGATACTGT TCTGTTACTG TTATTCCTTT	3723

TATGGTCTTC TTGAGACTTA AGTTTGTAGA ATTAAATTC CCTAGAGCTG GAGATAATGT 3783  
TTAGAGAATT AGGCCAATAA ATTT 3807

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Thr	Trp	Ile	Leu	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	Leu	Leu	Phe	Asn	Pro	
-20					-15					-10					-5	
Leu	Val	Lys	Thr	Glu	Gly	Ile	Cys	Arg	Asn	Arg	Val	Thr	Asn	Asn	Val	
				1				5					10			
Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	Lys	Asp	Tyr	Met	Ile	
		15					20					25				
Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	Pro	Ser	His	Cys	Trp	
	30					35					40					
Ile	Ser	Glu	Met	Val	Val	Gln	Leu	Ser	Asp	Ser	Leu	Thr	Asp	Leu	Leu	
45					50					55					60	
Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	
				65					70					75		
Asp	Lys	Leu	Val	Asn	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	Val	Lys	Glu	
			80					85					90			
Asn	Ser	Ser	Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	Ser	Pro	Glu	Pro	Arg	
		95					100					105				
Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile	Asp	
	110					115					120					
Ala	Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	Ser	Asp	Cys	Val	Val	
125					130					135					140	
Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Ile	Pro	Glu	Ser	Val	Ser	Gln	Asn	
			145						150					155		
His	Leu	Cys	Tyr	Pro	Leu	Leu	Gln	Pro	Ala	Pro	Leu	Gly	Met	Thr	Ala	
			160				165						170			
Val	Ala	Val														
			175													

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 17..640

(ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 92..640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAGCTTGCCT TTCCTT ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC	49
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys	
-25 -20 -15	
ATT TAT CTT CAG CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG	97
Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly	
-10 -5 1	
ATC TGC AGG AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG	145
Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu	
5 10 15	
GTG GCA AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC	193
Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro	
20 25 30	
GGG ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA	241
Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val	
35 40 45 50	
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT	289
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile	
55 60 65	
TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA	337
Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile	
70 75 80	
GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT AAG GAT CTA	385
Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu	
85 90 95	
AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT ACT CCT GAA GAA	433
Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu	
100 105 110	
TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC TTC AAG GAC TTT GTA	481
Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val	
115 120 125 130	
GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT TCT TCA ACA TTA AGT CCT	529
Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro	
135 140 145	
GAG AAA GAT TCC AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA CCC CCT	577
Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro	
150 155 160	
GTT GCA GCC AGC TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGT AAG	625
Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser Lys	
165 170 175	
TAC ATA TAT CTG ATT TAATGCATGC ATGGCTCCAA TTAGCACCTA TAGGAGTATT	680
Tyr Ile Tyr Leu Ile	
180	

GCATGGGCTT TCAAGGAAAC TTCTACATTT ATTATTATTG ATACTGTTCT GTTACTGTTA	740
TTCCTTTTAT GGTCTTCTTG AGACTTAAGT TTGTAGAATT AAATTTCCCT AGAGCTGGAG	800
ATAATGTTTA GAGAATTAGG	820

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 208 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Leu	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	-25	-20	-15	-10
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Glu	Gly	Ile	Cys	Arg	Asn	Arg	-5	1	5	
Val	Thr	Asn	Asn	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	10	15	20	
Lys	Asp	Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	25	30	35	
Pro	Ser	His	Cys	Trp	Ile	Ser	Glu	Met	Val	Val	Gln	Leu	Ser	Asp	Ser	40	45	50	55
Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	60	65	70	
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	Asn	Ile	Val	Asp	Asp	Leu	Val	75	80	85	
Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	90	95	100	
Ser	Pro	Glu	Pro	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	105	110	115	
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	120	125	130	135
Ser	Asp	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	140	145	150	
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	155	160	165	
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Ser	Lys	Tyr	Ile	Tyr	Leu	Ile	170	175	180	

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5864 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521,  
3932..4088, 4314..4397, 4778..4887, 5208..5275,  
5677..5713)

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932  
..4088, 4314..4397, 4778..4887, 5208..5275, 5677  
..5713)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GAGCTCCGAG CCCTCTCTGG CGCGCGAGGT ATTTCTGCTG TNCCCGGGGG TGCCAGGTGA	60
GCCCCAGCGG ATCCGGGAGG GTAAGCTGGG ACTCCTCGCG AGCAGTAGCT GCAGGGTACC	120
AAGCTTCGCC CTCTGCGTCC CCGCGCCTTC GCGGTCTCCC GCCAGTGCAG GTCCGGGGGCC	180
CCCAGGCGAG CGGACAAGGT TGGCCTAATC TGCCAAACTT CTGGGGCATT TACCGTGCTC	240
TGGCCGCCCT CCCGATTCTT CCCTCCGCGC CCTTGCTGCTC TTCTCGCCTA CCCC GGCTC	300
CGGAAGGGAA GGAGGCGTGT CCGGAGCAGG CGGGCGGGAA CTGTATAAAA GCGCCGGCGG	360
CTCAGCAGCC GGCTTCGCTC GCCGCTCGC GCCGAGACTA GAAGCGCTGC GGGGAAGCAGG	420
GACAGTGGAG AGGGCGCTGC GCTCGGGCTA CCCAATGCGT GGACTATCTG CCGCCGCTGT	480
TCGTGCAATA TGCTGGAGCT CCAGAACAGC TAAACGGAGT CGCCACACCA CTGTTTGTGC	540
TGGATCGCAC CGCTGCCTTT CTT ATG AAG AAG ACA CAA GTGAGTAGGG	589
Met Lys Lys Thr Gln	
-25	
CGCGCCCGGG AGCTCCCAGG CTCTCCAGGA AAAATCGCGC CCGGTGCCCC GGGGAAGCCG	649
GCGCTCCCTG GGACTTGCAG CTGGGGCGTG CAGGGCTGTG CCTGCCGGGT GAGACAAGAG	709
GATGCGGGGG AGGCCGCGT GGTGTGTGAT CCCGAGCCGA GCCGNNTGAG CCAGGGAGAA	769
AAGGAGTGGG AGTACTGAGA GGGAGCCAGT GTCAAGTTTG GAGCCTCAGC AGTTAAGTTT	829
TGAGCTGTCA GTCGGAAACC GTAATCCCG TCTGGTGGA AGATTGGCTT TTNGNCCACG	889
GAATGTAAGT TATCACAGAT ACTACAAAGA TAAATCAGTT GCACAAGTTC TTGAAACTCT	949
ACAGTGTAAT AAGGAAAAAT AAGTCATGCA TAAAAGCAAC TATAATACAT AATAGAAAAT	1009
GTTATTTTCA AGCCGATGTG TAGGTTATGT GTGTTGAGA GAGAGAGAGA GAAGACAGAT	1069
TACTTTCTGC TAGGGTTCAA GAATGCCTTC CTGTTGGCTA AGGAAATATT TTCCTTAAGT	1129
GGCTAAAAAG CTGTGTTTCA AAATATTCTT TTGATGTCTC ACAAATTCAG TGGAATTCTC	1189
TTAGGTCTAA AAATATACAT CTCTCTCACT TTAAGTTGGT GTGCTATTGT AGATTATTGG	1249
ATTAAAGCAC TGCTCAGGGA TTATGCTGCT TCTTGCCAAG CAGTCTACAT TTAAAGTAGA	1309
AATAAGATGT TTCTTTTGGT GCCATAAGGT ATACATTTTA TGCATTCTCT AGTTTTTAGA	1369
AGATACCCTA AGGGCTAAGT CTTTAACATG CTGCTACAAG TTTATTCCTA ATTGCCATTG	1429
GGAAATTGGC TGAAGAAAGT TTTTAACAAA AGTTAACAAAT ATTGTCATTG AGAGAATAAT	1489

TCAAAATGGA TTTTAACTAA AAGCTTTTAA AAACCTTTGGT GAGCATAGCT TGAATGCGTA	1549
ATATTTAATT GCATTTAAGC CAATAACATA TATTAGACTG GTCTTTTTGT GCATCAAGGC	1609
ATTAGATGTT AAAAGTTTGA ATGATTACAG ATCTTAACTG ATGATCACCA AGCAATTTTT	1669
CTGTTTTTCAT TTAG ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG CTG CTC Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu -20 -15 -10	1719
CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT CGT GTG Leu Phe Asn Asn Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val -5 1 5	1767
ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTAAGTAAGG AATGCTTTAC Thr Asn Asn Val Lys Asp Val Thr Lys Leu 10 15	1817
CGTGCTGTGT AAAAAAGAGC TGTGGCTCTT TTTCTGTGC TTGTTGATAA AAGATTTAGA	1877
TTTTTCTTGC CCCAAAGTAA TGTTTTCTTA AAGTGGGGAA AGTAATCACT GGGTTACAAT	1937
AAAGGGTTTA TAGAAAGCAG GTAGTGAGAT ATTTAGGGTC ATGGATAATT TGTTGGTAAA	1997
ACTGGCTAGT TGCACACCAC TGCTGTGACT GCTTCTTTGC TGGTCTTCTC CCCATCCTTC	2057
ATAGGCAGTG AAGGACCTTG GAGAGTTCGC TGTGTGCTGA TGGGCTTGCC CCAGCTTGTT	2117
CCCCATAATC TCTCCAGTGG GTTTCCAGC ATGTTCTATT CCCCTTCACA TGTCTTCTTA	2177
CTCTTCTTTA AAAAGCCTAA CGAAAGGAAA TCTGAAATGG CTATTCTCCC AATTCAATCA	2237
GCAGGAAGAC CCTGTCACAT GTCAGTGGGT GTTTGCTCCT TCAGGGAACA TAGAGAGGTG	2297
ATTCATTGCC CACATGTTGA AGGGACTCAT CTCCCTGGTT TGTCACATTG AACTCTTCCC	2357
TCAGCGAAAG CATTTGCATT GCTTCCCGAA TTCCAAGATC ACAGGTGGAA GCTGAAATTC	2417
AGATCATGTT TCCAAACTC AGTAGGTTAT ACCTAGCCAG GCATAACTGA ATTTGGAGTC	2477
TAAAAGATCT GTATTATCAC TTTTTTATTT TGAAGGATGC CTTTGTATTA CAGAGGGAAA	2537
TCAAGGATTA AAAATCAATA TACATGTAAA TATTGAAATT CATTGGTAAC TTTAAAAAGC	2597
ACAACAGTTT TGTGTGCTTT TCTCCAAAGC ACTACAAATA TGATTAATTG ATGTATAAGA	2657
ATTTTCTTAT GGAATTTTTT TTTTGTCTC TGTAG GTG GCA AAT CTT CCA AAA Val Ala Asn Leu Pro Lys 20	2710
GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT TTG Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu 25 30 35	2755
GTATGTAAAC TACATTTCTG AGTTTCATTT TAGTAGCTCA TAGAAGAAAT GGGATCATTC	2815
ATATTGAGAT AGTACACTAG CTGCTATTTA GGAGCTTGCT TATTGTCAGG ATTTGAAGAA	2875
TTTATCTTTG GAATTTGACT TGCAGGCTTT TTTTCCCCC TCTTCTGTGTT ACAAGAGTCC	2935
CTCCTCTAT TACAATAGTC CCTCCTCCTC CTGTCACACT AGTCCCTTCT CTTCTGTGTTA	2995
CAATAACCCC TGTCCCTCCTA TTACAACATT TTAAGTAATG TAATATTAAT TTTAAAAATC	3055
TGGCCAGGCA CGGTGGTTCA TGCTTGTAAT CCCAGCACAT TGGGAAGCTG AGACGGGTGG	3115



ATCATTTGAG GTCAGGAAGT TTGAGACAGC CTGGCCAACA TGGTGAAACT TCCTCTCTAC	3175
TAAAAATAAA AAAGTAGCCA GGCATGGTGG CAGGCACTTG TAATCTGAGC TACTCGAGAG	3235
GCTGAGGCAG GAGAATCACT TGAGTAACTA AAACGATAGC TTTGAAGAGT ACTCCGAGTT	3295
TTATGGCACT TACTTATTAA AATAGCTGTT TTGTCTCTTT TTTCATATCT TGCAG CCA	3353
	Pro 40
AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC AGC TTG	3401
Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser Leu	
	45 50 55
ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG AGT AAT	3449
Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn	
	60 65 70
TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT GTG GAG	3497
Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val Glu	
	75 80 85
TGC GTG AAA GAA AAC TCA TCT AAG GTAACCTTGT GTTCATTGGG ATTATTTTTC	3551
Cys Val Lys Glu Asn Ser Ser Lys	
	90 95
ATTACGCTTC TCTAAAAACC CATGCTTCTT GGTGCTGTTG GGGAAAATGA GGCACCTTTA	3611
TTTATGATAT TTTGATTGTA TAACTTCAA ATTTAAAAAT CTTGTTTCAGA TGAGCAAAGA	3671
AAACAAGTAT TTGCAGTTAT ACTGCAATAC TGAAGTGCAC TATTCTTGTG TTTACTGCCC	3731
CAGATTCAAC TTGTGATCCC ACTGGGATCA CTACCCTGCA TTACCAATCT GAATTACATA	3791
CGTTAAAACA GCCATCTAAA AGTGCTAGTT GTAAGAGTCT AAATACTTGA ATCTTTGAGA	3851
GACATATTTA TAGTCCATTA TCTTCACCTC AGTTAAGTCT GAAGACTATT TGAAAAATGT	3911
AATCCTATTT TTTCTTCTAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA	3961
Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu	
	100 105
CCC AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC	4009
Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser	
	110 115 120
ATT GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT	4057
Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys	
	125 130 135
GTG GTT TCT TCA ACA TTA AGT CCT GAG AAA G GTAAGACATG TAAGCATTTT	4108
Val Val Ser Ser Thr Leu Ser Pro Glu Lys	
	140 145
CAGTTCAAAT GTAAACAACA AACTTAAATC TTCCCTATGT AGTAAGAATC TACCTCTGTG	4168
TTAAGCTGTA GCAAGATACA TGCATGTACG TCTAAAAAAA AGCAGATATC AATAGCACAG	4228
AAGAACTAA TGATTGTAGA TTTGTGGGCT CTATAACTCA TACAAATCAC CATATAACAC	4288
TGACACATTA TTGCTTTCTA TTTAG AT TCC AGA GTC AGT GTC ACA AAA CCA	4339
Asp Ser Arg Val Ser Val Thr Lys Pro	
	150 155
TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT GAC AGC AGT	4387

Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser	
160 165 170	
AGC AGT AAT A GTAAGTACAT ATATCTGATT TAATGCATGC ATGGCTCCAA	4437
Ser Ser Asn	
175	
TTAGCACCTA TAGGAGTATT GCATGGGCTT TCAAGGAAAC TTCTACATTT ATTATTATTG	4497
ATACTGTTCT GTTACTGTTA TTCCTTTTAT GGTCTTCTTG AGACTTAAGT TTGTAGAATT	4557
AAATTTCCCT AGAGCTGGAG ATAATGTTTA GAGAATTAGG CCAATAAATT TTCTGCTGAG	4617
GTTATTTTAA ATAAGACATA AAATTAATTT TAGAAATATG ATTTATGCCT TTTGTTGAAT	4677
CATTAACATA TATACAGAAA CAGTTAAAAC AACCACAGCA TAAGAGAAAA ACTTCTAGAA	4737
TGGATATGCT GTATTCATCA GTGTGTTCTT TAAATTATAG GG AAG GCC AAA AAT	4791
Arg Lys Ala Lys Asn	
180	
CCC CCT GGA GAC TCC AGC CTA CAC TGG CCA GCC ATG GCA TTG CCA GCA	4839
Pro Pro Gly Asp Ser Ser Leu His Trp Pro Ala Met Ala Leu Pro Ala	
185 190 195	
TTG TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG	4887
Leu Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys	
200 205 210	
GTAAGTGGTA CCATTCCTTT TTTTAAAAAT ATGCTATGTT TACATAAATT ATCATCTTTT	4947
TTTCTCAAG AAATGATCCT TTAAGAAAAC AGTGAATCTA CCTTAGCTTA TACTAAACAA	5007
AATTTAAATT TTATAAGTT TCCTGTTTCT CATTATGTCT GGAGACAATC CCTCTAGCTG	5067
ATAATTCACG CTTAAGAATT AGGAACTAAA ACTGTTATTG GAGTTATTGC CATAAAAGAT	5127
AAAAGTGGAG TCCACTTACC TCTTAAATAT TAGACCATTC ATTGATTATT TTACAGTATA	5187
TGTCTTTCTT CTTTTTCCAG AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT	5237
Lys Arg Gln Pro Ser Leu Thr Arg Ala Val	
215 220	
GAA AAT ATA CAA ATT AAT GAA GAG GAT AAT GAG ATA AG GTATTTTGTT	5285
Glu Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile Ser	
225 230 235	
TTGCTAAATG TGTGCCCAAT CAAGCATGAC ATTGCCATTT CACACACTGT GTACCTGCCC	5345
ATAATGTCTT TAAGAAGTCC TTCACTCATG ACAGTAGCTC CTAACCAGTG AGTCCCAACT	5405
CTATCCATGT TTCTGATGTC TCACTCTCTC TTCGTATGTG TATATGCATA TACAGAGAAA	5465
GAAATGTTTT AACTACTTGG AAAGACTACC TTAAGACAAA TGAAGTCTTC CCTCTTCCCT	5525
ATAGTAATAA GAAGGTAGGC TCCCCATTC AATTTTGCAA TCTTCTGCTA CTATATTTAC	5585
AGAAAAGCTG CCTTTTACAA TGCCGAGATC ATGGTGTACC TCAGAATCTC TGACCAAGAG	5645
CAAATAAGCA TTTTTTCTTA TTGTTTTTCA G T ATG TTG CAA GAG AAA GAG AGA	5698
Met Leu Gln Glu Lys Glu Arg	
240	
GAG TTT CAA GAA GTG TAATTGTGGC TTGTATCAAC ACTGTTACTT TCGTACATTG	5753
Glu Phe Gln Glu Val	
245	

GTAAGTTTTT TTCTTCTTTC CTTTTTTTTT CTTTTTTTTTA TTATACTTTA AGTTCTAGGG 5813  
TACATGTGCA CAATGTGCAG GTTTGTTACG TATGTTTACA TGTGCCATGT T 5864

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Leu	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	-25	-20	-15	-10
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Glu	Gly	Ile	Cys	Arg	Asn	Arg	-5	1	5	
Val	Thr	Asn	Asn	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	10	15	20	
Lys	Asp	Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	25	30	35	
Pro	Ser	His	Cys	Trp	Ile	Ser	Glu	Met	Val	Val	Gln	Leu	Ser	Asp	Ser	40	45	50	55
Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	60	65	70	
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	Asn	Ile	Val	Asp	Asp	Leu	Val	75	80	85	
Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	90	95	100	
Ser	Pro	Glu	Pro	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	105	110	115	
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	120	125	130	135
Ser	Asp	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	140	145	150	
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	155	160	165	
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Lys	Asn	Pro	Pro	170	175	180	
Gly	Asp	Ser	Ser	Leu	His	Trp	Pro	Ala	Met	Ala	Leu	Pro	Ala	Leu	Phe	185	190	195	
Ser	Leu	Ile	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Arg	200	205	210	215
Gln	Pro	Ser	Leu	Thr	Arg	Ala	Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	Glu	220	225	230	
Asp	Asn	Glu	Ile	Ser	Met	Leu	Gln	Glu	Lys	Glu	Arg	Glu	Phe	Gln	Glu	235	240	245	

Val

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 273 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Leu	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	
1			5						10					15		
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Glu	Gly	Ile	Cys	Arg	Asn	Arg	
			20					25					30			
Val	Thr	Asn	Asn	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	
		35				40						45				
Lys	Asp	Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	
	50					55					60					
Pro	Ser	His	Cys	Trp	Ile	Ser	Glu	Met	Val	Val	Gln	Leu	Ser	Asp	Ser	
65					70					75					80	
Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	
			85						90					95		
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	Asn	Ile	Val	Asp	Asp	Leu	Val	
			100					105					110			
Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	
		115					120					125				
Ser	Pro	Glu	Pro	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	
	130					135					140					
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	
145					150					155					160	
Ser	Asp	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	
			165						170					175		
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	
			180					185					190			
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Lys	Asn	Pro	Pro	
		195					200					205				
Gly	Asp	Ser	Ser	Leu	His	Trp	Ala	Ala	Met	Ala	Leu	Pro	Ala	Leu	Phe	
	210					215					220					
Ser	Leu	Ile	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Arg	
225					230				235						240	
Gln	Pro	Ser	Leu	Thr	Arg	Ala	Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	Glu	
			245						250					255		
Asp	Asn	Glu	Ile	Ser	Met	Leu	Gln	Glu	Lys	Glu	Arg	Glu	Phe	Gln	Glu	
			260					265					270			

(2) INFORMATION FOR SEO ID NO:50:

(i) SEOUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu  
1 5 10 15

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg  
20 25 30

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro  
35 40 45

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu  
50 55 60

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser  
65 70 75 80

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
85 90 95

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val  
100 105 110

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys  
115 120 125

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe  
130 135 140

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Ala Val Ala Ser Glu Thr  
145 150 155 160

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg  
165 170 175

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser  
180 185 190

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Thr  
195 200 205

Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Phe Phe  
210 215 220

Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg  
225 230 235 240

Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
245 250 255

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu  
260 265 270

Val

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Ile	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	1	5	10	15
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Lys	Gly	Ile	Cys	Gly	Lys	Arg	20	25	30	
Val	Thr	Asp	Asp	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	35	40	45	
Lys	Asp	Tyr	Lys	Ile	Ala	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	50	55	60	
Pro	Ser	His	Cys	Trp	Ile	Ser	Val	Met	Val	Glu	Gln	Leu	Ser	Val	Ser	65	70	75	
Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	85	90	95	
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	Lys	Ile	Val	Asp	Asp	Leu	Val	100	105	110	
Glu	Cys	Thr	Glu	Gly	Tyr	Ser	Phe	Glu	Asn	Val	Lys	Lys	Ala	Pro	Lys	115	120	125	
Ser	Pro	Glu	Leu	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	130	135	140	
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Leu	Glu	Thr	Val	Ala	Ser	Lys	145	150	155	
Ser	Ser	Glu	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Asp	Lys	Asp	Ser	165	170	175	
Arg	Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	180	185	190	
Ser	Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Ser	Asn	Ser	195	200	205	
Ile	Gly	Asp	Ser	Asn	Leu	Gln	Trp	Ala	Ala	Met	Ala	Leu	Pro	Ala	Phe	210	215	220	
Phe	Ser	Leu	Val	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	225	230	235	
Lys	Gln	Pro	Asn	Leu	Thr	Arg	Thr	Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	245	250	255	
Glu	Asp	Asn	Glu	Ile	Ser	Met	Leu	Gln	Glu	Lys	Glu	Arg	Glu	Phe	Gln	260	265	270	

Glu Val

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met	Lys	Thr	Gln	Thr	Trp	Ile	Val	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	Leu	1	5	10	15
Phe	Asn	Pro	Leu	Val	Lys	Thr	Lys	Gly	Leu	Cys	Arg	Asn	Arg	Val	Thr	20	25	30	
Asp	Asp	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	Lys	Asp	35	40	45	
Tyr	Lys	Ile	Ala	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	Pro	Ser	50	55	60	
His	Cys	Trp	Ile	Ser	Val	Met	Val	Glu	Gln	Leu	Ser	Val	Ser	Leu	Thr	65	70	75	
Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	85	90	95	
Ser	Ile	Ile	Asp	Lys	Leu	Val	Lys	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	100	105	110	
Val	Glu	Gly	His	Ser	Ser	Glu	Asn	Val	Lys	Lys	Ser	Ser	Lys	Ser	Pro	115	120	125	
Glu	Pro	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	130	135	140	
Ser	Ile	Asp	Ala	Phe	Lys	Asp	Leu	Glu	Met	Val	Ala	Ser	Lys	Thr	Ser	145	150	155	
Glu	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	Val	165	170	175	
Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	Leu	180	185	190	
Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Thr	Asn	Pro	Ile	Glu	Asp	195	200	205	
Ser	Ser	Ile	Gln	Trp	Ala	Val	Met	Ala	Leu	Pro	Ala	Cys	Phe	Ser	Leu	210	215	220	
Val	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Phe	Tyr	Trp	Lys	Lys	Lys	Gln	Pro	225	230	235	
Asn	Leu	Thr	Arg	Thr	Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	Glu	Asp	Asn	245	250	255	
Glu	Ile	Ser	Met	Leu	Gln	Glu	Lys	Glu	Arg	Glu	Phe	Gln	Glu	Val	260	265	270		

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Ile	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	1	5	10	15
Leu	Leu	Phe	Asn	Pro	Leu	Val	His	Thr	Gln	Gly	Ile	Cys	Ser	Asn	Arg	20	25	30	
Val	Thr	Asp	Asp	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	35	40	45	
Lys	Asp	Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	50	55	60	
Pro	Ser	His	Cys	Trp	Ile	Ser	Glu	Met	Val	Glu	Gln	Leu	Ser	Val	Ser	65	70	75	80
Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	85	90	95	
Asn	Tyr	Cys	Ile	Ile	Asp	Lys	Leu	Val	Lys	Ile	Val	Asp	Asp	Leu	Val	100	105	110	
Glu	Cys	Met	Glu	His	Ser	Ser	Glu	Asn	Val	Lys	Lys	Ser	Ser	Lys	Ser	115	120	125	
Pro	Glu	Pro	Arg	Gln	Phe	Thr	Pro	Glu	Lys	Phe	Phe	Gly	Ile	Phe	Asn	130	135	140	
Lys	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Leu	Glu	Ile	Val	Ala	Ser	Lys	Met	145	150	155	160
Ser	Glu	Cys	Val	Ile	Ser	Ser	Thr	Ser	Ser	Pro	Glu	Lys	Asp	Ser	Arg	165	170	175	
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	180	185	190	
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Ser	Asn	Ser	Ile	195	200	205	
Glu	Asp	Ser	Ser	Leu	Gln	Trp	Ala	Ala	Val	Ala	Leu	Pro	Ala	Phe	Phe	210	215	220	
Ser	Leu	Val	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Phe	Tyr	Trp	Lys	Lys	Lys	225	230	235	240
Gln	Pro	Asn	Leu	Thr	Arg	Thr	Val	Glu	Asn	Arg	Gln	Ile	Asn	Glu	Glu	245	250	255	
Asp	Asn	Glu	Ile	Ser	Met	Leu	Gln	Glu	Lys	Glu	Arg	Glu	Phe	Gln	Glu	260	265	270	
Val																			



(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 273 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Ile	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	
1				5					10					15		
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Gln	Glu	Ile	Cys	Arg	Asn	Pro	
			20					25					30			
Val	Thr	Asp	Asn	Val	Lys	Asp	Ile	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	
		35					40					45				
Asn	Asp	Tyr	Met	Ile	Thr	Leu	Asn	Tyr	Val	Ala	Gly	Met	Asp	Val	Leu	
	50					55					60					
Pro	Ser	His	Cys	Trp	Leu	Arg	Asp	Met	Val	Thr	His	Leu	Ser	Val	Ser	
65					70					75					80	
Leu	Thr	Thr	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	
			85						90					95		
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Gly	Lys	Ile	Val	Asp	Asp	Leu	Val	
		100						105					110			
Ala	Cys	Met	Glu	Glu	Asn	Ala	Pro	Leu	Asn	Val	Lys	Glu	Ser	Leu	Lys	
		115					120					125				
Lys	Pro	Glu	Thr	Arg	Asn	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Ser	Ile	Phe	
	130					135					140					
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Met	Val	Ala	Ser	Asp	Thr	
145					150					155					160	
Ser	Asp	Cys	Val	Leu	Ser	Ser	Thr	Leu	Gly	Pro	Glu	Lys	Asp	Ser	Arg	
			165						170					175		
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	
		180						185					190			
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Ala	Lys	Ser	Pro	
		195					200					205				
Glu	Asp	Pro	Gly	Leu	Gln	Trp	Thr	Ala	Met	Ala	Leu	Pro	Ala	Leu	Ile	
	210					215					220					
Ser	Leu	Val	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Lys	
225					230					235					240	
Gln	Ser	Ser	Leu	Thr	Arg	Ala	Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	Glu	
			245						250					255		
Asp	Asn	Glu	Ile	Ser	Met	Leu	Gln	Gln	Lys	Glu	Arg	Glu	Phe	Gln	Glu	
		260						265					270			

Val

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Thr 1	Trp	Ile	Ile	Thr 5	Cys	Phe	Cys	Leu	Gln 10	Leu	Leu	Leu	Leu	Asn 15	Pro
Leu	Val	Lys	Ala 20	Gln	Ser	Ser	Cys	Gly 25	Asn	Pro	Val	Thr	Asp 30	Asp	Val
Asn	Asp	Ile 35	Ala	Lys	Leu	Val	Gly 40	Asn	Leu	Pro	Asn	Asp 45	Tyr	Leu	Ile
Thr	Leu 50	Lys	Tyr	Val	Pro	Lys 55	Met	Asp	Ser	Leu	Pro 60	Asn	His	Cys	Trp
Leu 65	His	Leu	Met	Val	Pro 70	Glu	Phe	Ser	Arg	Ser 75	Leu	His	Asn	Leu	Leu 80
Gln	Lys	Phe	Ser	Asp 85	Ile	Ser	Asp	Met	Ser 90	Asp	Val	Leu	Ser	Asn 95	Tyr
Ser	Ile	Ile	Asn 100	Asn	Leu	Thr	Arg	Ile 105	Ile	Asn	Asp	Leu	Met 110	Ala	Cys
Leu	Ala	Phe 115	Asp	Lys	Asn	Lys	Asp 120	Phe	Ile	Lys	Glu	Asn 125	Gly	Leu	His
Tyr	Glu 130	Glu	Asp	Arg	Phe	Ile 135	Pro	Glu	Asn	Phe	Phe 140	Arg	Leu	Phe	Asn
Ser 145	Thr	Ile	Glu	Val	Tyr 150	Lys	Glu	Phe	Ala	Asp 155	Ser	Leu	Asp	Lys	Asn 160
Asp	Cys	Ile	Met	Pro 165	Ser	Thr	Val	Glu	Thr 170	Pro	Glu	Asn	Asp	Ser 175	Arg
Val	Ala	Val	Thr 180	Lys	Thr	Ile	Ser	Phe 185	Pro	Pro	Val	Ala	Ala 190	Ser	Ser
Leu	Arg	Asn 195	Asp	Ser	Ile	Gly	Ser 200	Asn	Thr	Ser	Ser	Asn 205	Ser	Asn	Lys
Glu	Ala 210	Leu	Gly	Phe	Ile	Ser 215	Ser	Ser	Ser	Leu	Gln 220	Gly	Ile	Ser	Ile
Ala 225	Leu	Thr	Ser	Leu	Leu 230	Ser	Leu	Leu	Ile	Gly 235	Phe	Ile	Leu	Gly	Ala 240
Ile	Tyr	Trp	Lys	Lys 245	Thr	His	Pro	Lys	Ser 250	Arg	Pro	Glu	Ser	Asn 255	Glu
Thr	Ile	Gln	Cys 260	His	Gly	Cys	Gln	Glu 265	Glu	Asn	Glu	Ile	Ser 270	Met	Leu
Gln	Gln	Lys 275	Glu	Lys	Glu	His	Leu 280	Gln	Val						

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Ile	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	1	5	10	15
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Gly	Ile	Cys	Arg	Asn	Arg	Val	20	25	30	
Thr	Asp	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	Lys	Asp	35	40	45	
Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	Pro	Ser	50	55	60	
His	Cys	Trp	Ile	Ser	Glu	Met	Val	Glu	Gln	Leu	Ser	Val	Ser	Leu	Thr	65	70	75	80
Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	85	90	95	
Ser	Ile	Ile	Asp	Lys	Leu	Val	Lys	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	100	105	110	
Glu	Glu	Asn	Ser	Ser	Lys	Asn	Val	Lys	Lys	Ser	Lys	Ser	Pro	Glu	Pro	115	120	125	
Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile	130	135	140	
Asp	Ala	Phe	Lys	Asp	Phe	Met	Val	Ala	Ser	Lys	Thr	Ser	Asp	Cys	Val	145	150	155	160
Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	Val	Ser	Val	Thr	165	170	175	
Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	Leu	Arg	Asn	Asp	180	185	190	
Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Asn	Glu	Asp	Ser	Ser	Leu	Gln	Trp	195	200	205	
Ala	Ala	Met	Ala	Leu	Pro	Ala	Leu	Phe	Ser	Leu	Val	Ile	Gly	Phe	Ala	210	215	220	
Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Lys	Gln	Pro	Ser	Leu	Thr	Arg	Ala	225	230	235	240
Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	Glu	Asp	Asn	Glu	Ile	Ser	Met	Leu	245	250	255	
Gln	Glu	Lys	Glu	Arg	Glu	Phe	Gln	Glu	Val	260	265								

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(1..210, 223..258)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAA TTC TTC CGT ATC TTC AAC CGT TCC ATC GAC GCT TTC AAA GAC TTC	48
Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe	
1 5 10 15	
GTT GTT GCT TCC GAA ACC TCC GAC TGC GTT GTT TCC TCC ACC CTG TCT	96
Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser	
20 25 30	
CCG GAA AAA GAC TCC CGT GTT TCG GTT ACC AAA CCG TTC ATG CTG CCG	144
Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro	
35 40 45	
CCG GTT GCT GCT TCC TCC CTG CGT AAC GAC TCC TCC TCC TCC AAC TCC	192
Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser	
50 55 60	
AAA TAC ATC TAC CTG ATC TAATAGGATC CG GTT ACC AAA CCG TTC ATG	240
Lys Tyr Ile Tyr Leu Ile Val Thr Lys Pro Phe Met	
65 70 75	
CTG CCG CCG GTT GCT GCT TAATAGGATC C	269
Leu Pro Pro Val Ala Ala	
80	

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe	
1 5 10 15	
Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser	
20 25 30	
Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro	
35 40 45	
Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser	
50 55 60	
Lys Tyr Ile Tyr Leu Ile Val Thr Lys Pro Phe Met Leu Pro Pro Val	
65 70 75 80	
Ala Ala	

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 184..1002

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 259..1002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

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CCGCCTCGCG CCGAGACTAG AAGCGCTGCG GGAAGCAGGG ACAGTGGAGA GGGCGCTGCG      60
CTCGGGCTAC CCAATGCGTG GACTATCTGC CGCCGCTGTT CGTGCAATAT GCTGGAGCTC      120
CAGAACAGCT AAACGGAGTC GCCACACCAC TGTTTGTGCT GGATCGCAGC GCTGCCTTTC      180
CTT ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG      228
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
-25 -20 -15

CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT      276
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn
-10 -5 1 5

CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA AAT CTT      324
Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu
10 15 20

CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT      372
Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val
25 30 35

TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC      420
Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp
40 45 50

AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG      468
Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu
55 60 65 70

AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT      516
Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu
75 80 85

GTG GAG TGC GTG AAA GAA AAC TCA TCT AAG GAT CTA AAA AAA TCA TTC      564
Val Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe
90 95 100

AAG AGC CCA GAA CCC AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT      612
Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile
105 110 115

TTT AAT AGA TCC ATT GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA      660
Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu
120 125 130

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ACT AGT GAT TGT GTG GTT TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC	708
Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser	
135 140 145 150	
AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC	756
Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser	
155 160 165	
TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC	804
Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro	
170 175 180	
CCT GGA GAC TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG	852
Pro Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu	
185 190 195	
TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG	900
Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys	
200 205 210	
AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA	948
Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu	
215 220 225 230	
GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT CAA	996
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln	
235 240 245	
GAA GTG TAATTGTGGC TTGTATCAAC ACTGTTACTT TCGTACATTG GCTGGTAACA	1052
Glu Val	
GTTCATGTTT GCTTCATAAA TGAAGCAGCT TTAAACAAAT TCATATTCTG TCTGGAGTGA	1112
CAGACCACAT CTTTATCTGT TCTTGCTACC CATGACTTTA TATGGATGAT TCAGAAATTG	1172
GAACAGAATG TTTTACTGTG AACTGGCAC TGAATTAATC ATCTATAAAG AAGAACTTGC	1232
ATGGAGCAGG ACTCTATTTT AAGGACTGCG GGACTTGGGT CTCATTTAGA ACTTGCAGCT	1292
GATGTTGGAA GAGAAAGCAC GTGTCTCAGA CTGCATGTAC CATTTCATG GCTCCAGAAA	1352
TGTCTAAATG CTGAAAAAAC ACCTAGCTTT ATTCTTCAGA TACAAACTGC AG	1404

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu	
-25 -20 -15 -10	
Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg	
-5 1 5	
Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro	
10 15 20	
Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu	
25 30 35	

Val

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1088 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

```
(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 151..885
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AGCAGGGACA GTGGAGAGGG CGCTGCGCTC GGGCTACCCA ATGCGTGGAC TATCTGCCGC 60  
CGCTGTTCGT GCAATATGCT GGAGCTCCAG AACAGCTAAA CGGAGTCGCC ACACCACTGT 120



TTGTGCTGGA	TCGCAGCGCT	GCCTTTCCTT	ATG	AAG	AAG	ACA	CAA	ACT	TGG	ATT							174
			Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile							
			-25														
CTC	ACT	TGC	ATT	TAT	CTT	CAG	CTG	CTC	CTA	TTT	AAT	CCT	CTC	GTC	AAA		222
Leu	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys		
		-15					-10					-5					
ACT	GAA	GGG	ATC	TGC	AGG	AAT	CGT	GTG	ACT	AAT	AAT	GTA	AAA	GAC	GTC		270
Thr	Glu	Gly	Ile	Cys	Arg	Asn	Arg	Val	Thr	Asn	Asn	Val	Lys	Asp	Val		
	1				5					10					15		
ACT	AAA	TTG	GTG	GCA	AAT	CTT	CCA	AAA	GAC	TAC	ATG	ATA	ACC	CTC	AAA		318
Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	Lys	Asp	Tyr	Met	Ile	Thr	Leu	Lys		
				20					25					30			
TAT	GTC	CCC	GGG	ATG	GAT	GTT	TTG	CCA	AGT	CAT	TGT	TGG	ATA	AGC	GAG		366
Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	Pro	Ser	His	Cys	Trp	Ile	Ser	Glu		
			35					40					45				
ATG	GTA	GTA	CAA	TTG	TCA	GAC	AGC	TTG	ACT	GAT	CTT	CTG	GAC	AAG	TTT		414
Met	Val	Val	Gln	Leu	Ser	Asp	Ser	Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe		
		50					55					60					
TCA	AAT	ATT	TCT	GAA	GGC	TTG	AGT	AAT	TAT	TCC	ATC	ATA	GAC	AAA	CTT		462
Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu		
	65					70					75						
GTG	AAT	ATA	GTG	GAT	GAC	CTT	GTG	GAG	TGC	GTG	AAA	GAA	AAC	TCA	TCT		510
Val	Asn	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser		
	80				85					90					95		
AAG	GAT	CTA	AAA	AAA	TCA	TTC	AAG	AGC	CCA	GAA	CCC	AGG	CTC	TTT	ACT		558
Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	Ser	Pro	Glu	Pro	Arg	Leu	Phe	Thr		
				100					105					110			
CCT	GAA	GAA	TTC	TTT	AGA	ATT	TTT	AAT	AGA	TCC	ATT	GAT	GCC	TTC	AAG		606
Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys		
			115					120					125				
GAC	TTT	GTA	GTG	GCA	TCT	GAA	ACT	AGT	GAT	TGT	GTG	GTT	TCT	TCA	ACA		654
Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	Ser	Asp	Cys	Val	Val	Ser	Ser	Thr		
		130					135					140					
TTA	AGT	CCT	GAG	AAA	GGG	AAG	GCC	AAA	AAT	CCC	CCT	GGA	GAC	TCC	AGC		702
Leu	Ser	Pro	Glu	Lys	Gly	Lys	Ala	Lys	Asn	Pro	Pro	Gly	Asp	Ser	Ser		
	145					150					155						
CTA	CAC	TGG	GCA	GCC	ATG	GCA	TTG	CCA	GCA	TTG	TTT	TCT	CTT	ATA	ATT		750
Leu	His	Trp	Ala	Ala	Met	Ala	Leu	Pro	Ala	Leu	Phe	Ser	Leu	Ile	Ile		
	160																

TGAAGCAGCT TTAAACAAAT TCATATTCTG TCTGGAGTGA CAGACCACAT CTTTATCTGT 1015  
TCTTGCTACC CATGACTTTA TATGGATGAT TCAGAAATTG GAACAGAATG TTTTACTGTG 1075  
AAACTGGCAC TGA 1088

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu  
-25 -20 -15 -10  
Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg  
-5 1 5  
Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro  
10 15 20  
Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu  
25 30 35  
Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser  
40 45 50 55  
Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
60 65 70  
Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val  
75 80 85  
Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys  
90 95 100  
Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe  
105 110 115  
Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr  
120 125 130 135  
Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Gly Lys Ala  
140 145 150  
Lys Asn Pro Pro Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu  
155 160 165  
Pro Ala Leu Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr  
170 175 180  
Trp Lys Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln  
185 190 195  
Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg  
200 205 210 215  
Glu Phe Gln Glu Val  
220

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Glu Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val Lys Asp Ile Thr  
1                      5                      10                      15  
Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr  
                    20                      25                      30  
Val Ala Gly Met Asp Val Leu Pro Ser His Xaa Trp Leu Arg Asp  
                    35                      40                      45

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ile Thr Thr Leu Asn Tyr Val Ala Gly Met  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Xaa Xaa Leu Gly Pro  
1                      5                      10                      15  
Glu Lys Asp Ser Arg Val Ser Val Xaa Lys  
                    20                      25

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met  
1 5 10

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Glu Asn Ala Pro Lys Asn Val Glu Ser Leu Lys Lys Pro Thr Arg  
1 5 10 15  
Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe Asp Arg Ser Ile Asp  
20 25 30

Ala

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Glu Ser Leu Lys Lys Pro Glu Thr Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Val Ser Val Xaa Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ile Val Asp Asp Leu Val Ala Ala Met Glu Glu Asn Ala Pro Lys  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe Xaa Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr Val  
1 5 10 15

Ala Gly Asp Asp Val Leu Pro Ser His Cys Trp Leu Arg  
20 25

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr Ser Asp  
1 5 10 15

Cys Val Leu Ser Xaa Xaa Leu Gly  
20

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe  
1 5 10 15

Phe Ser Ile Phe Xaa Arg  
20

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe  
1 5 10 15

Phe Ser Ile Phe Asp Arg  
20

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Asn Ala Pro Lys Asn Val Lys Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser Arg Val Ser Val Xaa Lys Pro Phe Met Leu Pro Pro Val Ala Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe  
1 5 10 15

Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala  
20 25 30

Ser Asp

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe  
1 5 10 15

Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala  
20 25 30

Ser Asp Thr Ser Asp  
35

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Leu Arg Asp Met Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu  
1 5 10 15

Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile  
20 25 30

Asp Lys Leu Gly Lys Ile Val Asp  
35 40

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Pro Val Ala Ala  
1

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCTGAGAAAG ATTCCAGAGTC

21

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTGCAGTTTG TATCTGAAG

19

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CATATAAAGT CATGGGTAG

19

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ACTTGTGTCT TCTTCATAAG GAAAGGC

27

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TGTACGAAAG TAACAGTGTT G

21

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ACTGCTCCTA TTTAATCCTC TC

22

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CACTGACTCT GGAATCTTTC TCA

23

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCGACCCGGA TCCCC

15

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TCGAGGGGAT CCGGG

15

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TCTTCTTCAT GCGGCGGCA AGCTT

25

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp	Ser	Arg	Val	Ser	Val	Xaa	Lys	Pro	Phe	Phe	Met	Leu	Pro	Pro	Val
1				5					10					15	

Ala Ala

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Asp	Ser	Arg	Val	Ser	Val	Thr	Lys	Pro	Phe	Phe	Met	Leu	Pro	Pro	Val
1				5					10					15	

Ala Ala

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CGATTTGATT CTAGAAGGAG GAATAACATA TGGTTAACGC GTTGAATTC GGTAC

55

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGAATTCCAA CGCGTTAACC ATATGTTATT CCTCCTTCTA GAATCAAAT

49

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TATGCAGGA

9

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GATCTCCTGC A

11

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TATGGAAGGT ATCTGCA

17

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GATACCTTCC A

11

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTCCTTATG

10

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCCGCCGCCA TG

12

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TCTTCTTCAT GCGGCGGCA AGCTT

25

Sub D1  
cont.